



MRALGPGLSLLCLVLALPALLPVPVAVRGVAETPTYTPWRDAETGERLVCAQCPPGTFVQR
 PCRRDSPPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEEARACHATHNRACRCRTGFF
 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSSSSSSSEQCQPHRNCTALGLA
 LNVPGSSSHDTLCTSTCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLQLALEAPE
 GWGPTPRAGRAALQLKLRRRLTELLGAQDQDALLVRLQLALRVARMPGLERSVRERFLPVH

FIG. 1

TCCGCAGGCGGACCGGGGGCAAAGGAGGTGGCATGTGCGTCAAGGCACAGCAGGGTCCTGT
 GTCCGCGCTGAGCCGCGCTCTCCCTGCTCCAGCAAGGACC
 ><Met {trans=1-s, dir=f, res=1}>
 ATGAGGGCGCTGGAGGGGCCAGGCCGTGTCGCTGCTGTGCCTGGTGTGGCGCTGCCTGCC
 CTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAAACACCCACCTACCCCTGGCGGGAC
 GCAGAGACAGGGGAGCGGCTGGTGTGCGCCAGTGCCCCCAGGCACCTTTGTGCAGCGG
 CCGTGCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAG
 TTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCTCTGCGGGGAGCGTGAGGAG
 GAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCTGCCGCTGCCGCACCGGCTTCTTC
 GCGCACGCTGGTTTTCTGCTTGAGCACGCATCGTGTCCACCTGGTGGCGGCGTGATTGCC
 CCGGGCACCCCGAGCCAGAACACGCAGTGCCAGCCGTGCCCCCAGGCACCTTCTCAGCC
 AGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCC
 CTCAATGTGCCAGGCTCTTCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCC
 CTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCT
 TTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCGGAG
 GGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCCTTGAGCTGAAGCTGCGTCGGCGG
 CTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGGCGCTGCTGCAGGCGCTG
 CGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC
 TGATCCTGGCCCCCTCTTATTTATTCTACATCCTTGGCACCCCACTTGCACTGAAAGAGG
 CTTTTTTTTTAAATAAGAAGAAATGAGGTTTNTTAAAAAAAAAAAAAAAAAAAAA

FIG. 2

GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCTCTGNNG
 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
 GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTTCTGCTTGAGAC
 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCGAGCCA
 GAACACGCAGTGCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCTGTGCACCAGCT
 GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
 CGTGCCGTCATCGACTTTGTGGCTTTCAGGACATCTCCAT

FIG. 3



SEQ ID NO: 4 128 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
SEQ ID NO: 5 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCNACTACACG
SEQ ID NO: 6 1 G
SEQ ID NO: 3 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG

SEQ ID NO: 4 178 CA-TTCTGGA ACTACCTGGAGCGC
SEQ ID NO: 5 51 CAGTTCTGGAANTA ACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNNG
SEQ ID NO: 6 2 CAGTTCTGGA ACTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGG
SEQ ID NO: 3 51 CAGTTCTGGAANTA ACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNNG

SEQ ID NO: 5 101 GGAGCNTGAGGAGGAGGCANGNGCTTGCCACGCCACCCACAACCGCGCCT
SEQ ID NO: 6 52 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
SEQ ID NO: 7 1 GAGGGGCCCCCAGGAGTGGTGGCCGGAGGTG
SEQ ID NO: 3 101 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT

SEQ ID NO: 5 151 GCNGCTGCAGCACCGGNTTCTTCGCGCACGCTGNNTTCTGCTTGAGGACAC
SEQ ID NO: 6 102 GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGAGGACAC
SEQ ID NO: 7 32 TGGCAGGGGT CAGGTTGCTGGTCCCAGCCTTGCAACCTGAGCTAGGACAC
SEQ ID NO: 3 151 GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGAGGACAC

SEQ ID NO: 5 201 GCATCGTGTCCACCTGGTGNCGGCGTGATTGCNCCGGGCACCCCCAGCCA
SEQ ID NO: 6 152 GCATCGTGTCCACCTGGTGNCGGCGTGATTNCCCCGGGCACCCCCAGCCA
SEQ ID NO: 7 82 CAGTTCCCCTGACCCTGTTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCA
SEQ ID NO: 8 1 GCATCGTGTCCACCTGGTGNCGGCGTGATTGCCCCGGGCACCCCCAGCCA
SEQ ID NO: 10 1 CTTGTCCACCTGGTGNCGGCGTGATTNCCC -GGGCACCCCCAGCCA
SEQ ID NO: 3 201 GCATCGTGTCCACCTGGTGNCGGCGTGATTGCCCCGGGCACCCCCAGCCA

SEQ ID NO: 5 251 GAACACGCA -TGCAAAGCCGTG
SEQ ID NO: 7 132 GAACACGCAGN -CC -AGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID NO: 8 51 GAACACGCAG -GCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID NO: 10 47 GAACACGCAGTGCC -AGCCNT -CCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID NO: 9 1 AGCNGTGCNCCNCAGGCACCTTCTCAGCCAGCAGT
SEQ ID NO: 3 251 GAACACGCAGTGCCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC

SEQ ID NO: 7 182 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO: 8 101 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO: 10 97 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO: 9 36 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO: 3 301 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT

SEQ ID NO: 7 232 GGCCCTCAATGTGCCAGGCTCTTCCCTCCCATGACACCCTGTGCACCAG
SEQ ID NO: 8 151 GGCCCTCAATGTGCCAGGCTCTTCCCTCCCATGACACCCTGTGCACCAGCT
SEQ ID NO: 10 147 GGCCCTCAATGTGCCAGGCTCTTCCCTCCCATGACACCCTGTGCACCAGCT
SEQ ID NO: 9 86 GGCCCTCAATGTGCCAGGCTCTTCCCTCCCATGACACGCTGTGCACCAGCT
SEQ ID NO: 3 351 GGCCCTCAATGTGCCAGGCTCTTCCCTCCCATGACACCCTGTGCACCAGCT

SEQ ID NO: 10 197 GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
SEQ ID NO: 9 136 GCACTGGCTTCCCCCTCAGCACCAGGGTANCAGGAGCTGAGGAGTGTGAG
SEQ ID NO: 3 401 GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG

SEQ ID NO: 10 247 CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT
SEQ ID NO: 9 186 CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT
SEQ ID NO: 3 451 CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT

FIG. 4



DNA30942	1	M R A L E G P G L S L L C L V L A L P A L L P V P A V R G V A E T P T Y P W R D . A E T G
htNFR2	1	M A P V A V W A A L A V G L E L W A A A H A L P A Q V A F T P V . A P E P G S T C R L R E Y Y D Q T
CRD 1		
DNA30942	45	E R L V C A Q C P P G T F V Q R P C R R D S P T T C G P C P P R H Y T Q F W N Y L E R C R Y C N V L
htNFR2	50	A Q M C C S K C S P G Q H A K V F C T K T S D T V C C D S C E D S T Y T Q L W N W V P E C L S C G S R
CRD 2		
DNA30942	95	C G E R E E A R A C H A T H N R A C R C R T G F F . . . A H A G . . F C L E H A S C P P G A G V
htNFR2	100	C S S D Q V E T Q A C T R E Q N R I C T C R P G W Y C A L S K Q E G C R L C A P L R K C R P G F G V
CRD 3		
DNA30942	139	I A P G T P S Q N T Q C Q P C P P G T F S A S S S S E Q C C Q P H R N C T A L G L A L N V P G S S S
htNFR2	150	A R P G T E T S D V V C K P C A P G T F S N T T S S T D I C R P H Q I C N V V A . . . I P G N A S
CRD 4		
DNA30942	189	H D T L C T S C T G F P L S T R V P G A E E C E R A V I D F V A F Q D I S I K R L Q R L L Q A L E A
htNFR2	196	R D A V C T S T S . . P T R S M A P G A V H L P Q P V S T R S Q H T Q P T P E P S T A P S T S F L L
CRD 4		
DNA30942	239	P E G W G P T P . . R A G R A A L Q L K L R R R L T E L L G A Q D G A L L V R L L Q A L R V A R M P
htNFR2	244	P M G P S P P A E G S T G D F A L P V G L I V G V T A L L G L L I I G V V N C V I M T Q V K K P L .
CRD 4		
DNA30942	287	G L E R S V R E R F L P V H
htNFR2	293	C L Q R E A K V P H L P A D K A R G T Q G P E Q Q H L L I T A P S S S S S L E S S A S A L D R R A
CRD 4		
htNFR2	343	P T R N Q P Q A P G V E A S G A G E A R A S T G S S D S S P G G H G T Q V N V T C I V N V C S S S D
CRD 4		
htNFR2	393	H S S Q C S S Q A S S T M G D T D S S P S E S P K D E Q V P F S K E E C A F R S Q L E T P E T L L G
CRD 4		
htNFR2	443	S T E E K P L P L G V P D A G M K P S

FIG. 5



DcR3 1 M R A L E G P G L S L C L V L A L P A L L P V A V R G V A 31
OPG 1 M N K L L C C A L V F L D L S I K W T T Q E T F P - - - - - 25

DcR3 32 E T P T Y P W R D A E T G E R L V C A Q C P P G T F V Q R P C 62
OPG 26 - - P K Y L H Y D E E T S H Q L L C D K C P P G T Y L K Q H C 54

DcR3 63 R R D S P T C G P C P P R R H Y T Q F W N Y L E R C R Y C N V 93
OPG 55 T A K W K T V C A P C P D H Y Y T D S W H T S D E C L Y C S P 85

DcR3 94 L C G E R E E A R A C H A T H N R A C R C R T G F F A H A G 124
OPG 86 V C K E L Q Y V K Q E C N R T H N R V C E C K E G R Y L E I E 116

DcR3 125 F C L E H A S C P P G A G V I A P G T P S Q N T Q C Q P C P P 155
OPG 117 F C L K H R S C P P G F G V V Q A G T P E R N T V C K R C P D 147

DcR3 156 G T F S A S S S S E Q C Q P H R N C T A L G L A L N V P G S 186
OPG 148 G F S N E T S S K A P C R K H T N C S V F G L L T Q K G N 178

DcR3 187 S S H D T L C T S C T G F P L S T R V P G A E E C E R A V I D 217
OPG 179 A T H D N I C S G N S E S T Q K C G I D - V T L C E E A F F R 208

DcR3 218 F V A F Q D I S I K R L Q R L L Q A L E A P E G W G P T - P R 247
OPG 209 E A V P T K F T P N W L S V L V D N L P G T K V N A E S V E R 239

DcR3 248 A G R A A L Q L K L R R R L T E L L G A Q D G A L - L V R L L 277
OPG 240 I K R Q H S S Q E Q T F Q L L K L W K H Q N K A Q D I V K K I 270

DcR3 278 Q A L R V A R M P G L E R S V R E R F L P V H 300
OPG 271 I Q D I D L C E N S V Q R H I G H A N L T F E 293...

FIG. 6

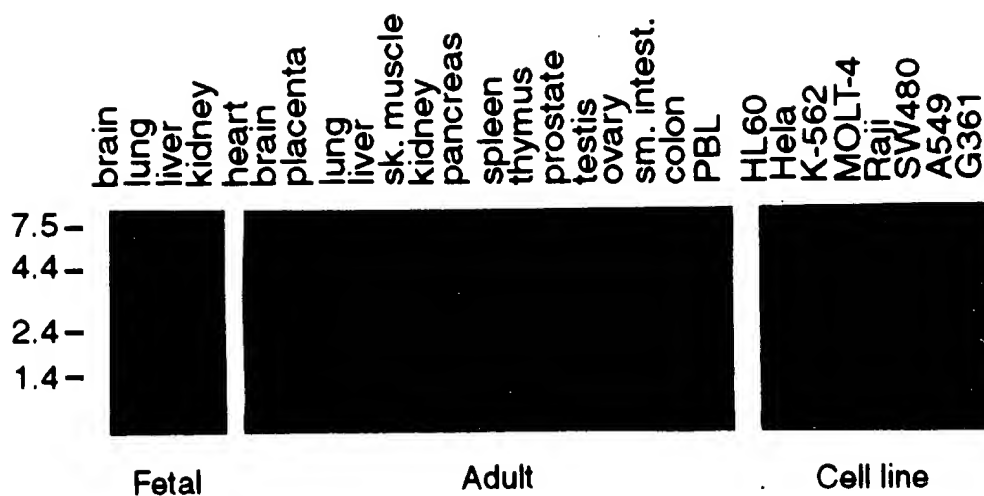


FIG. 7

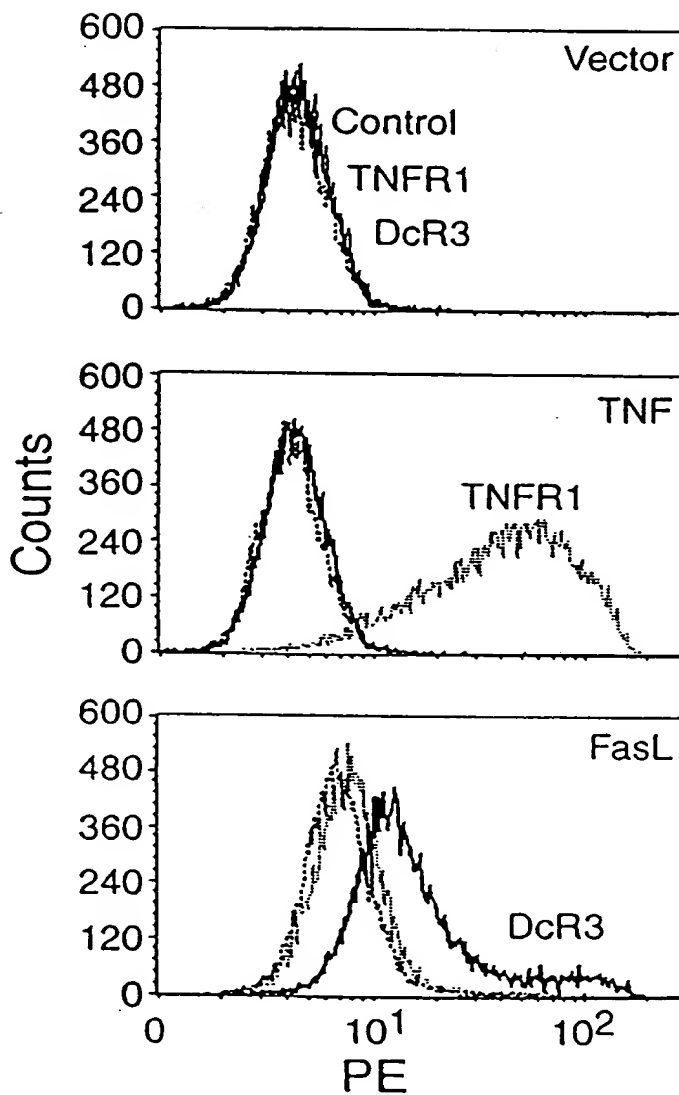


FIG. 8A

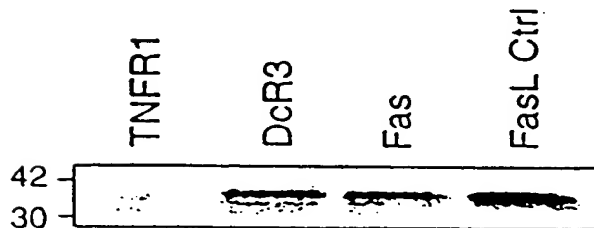


FIG. 8B

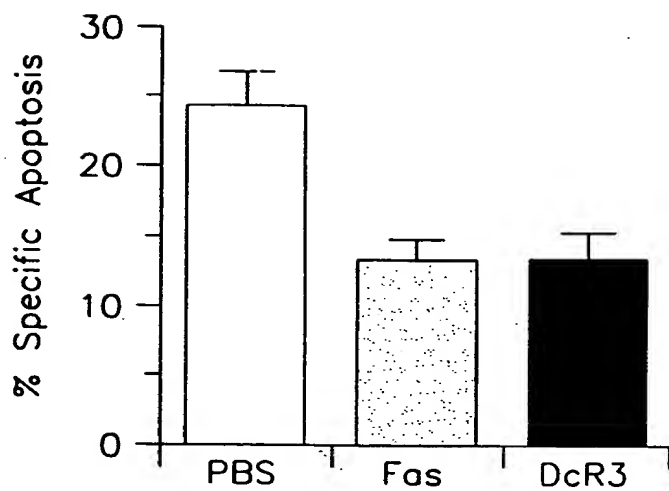


FIG. 9A

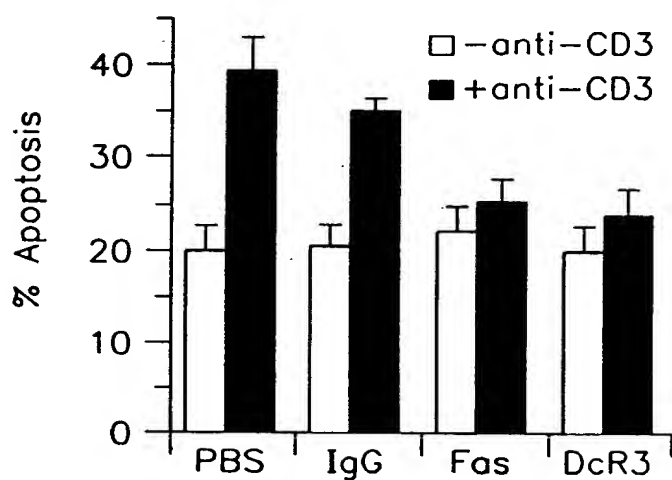


FIG. 9B

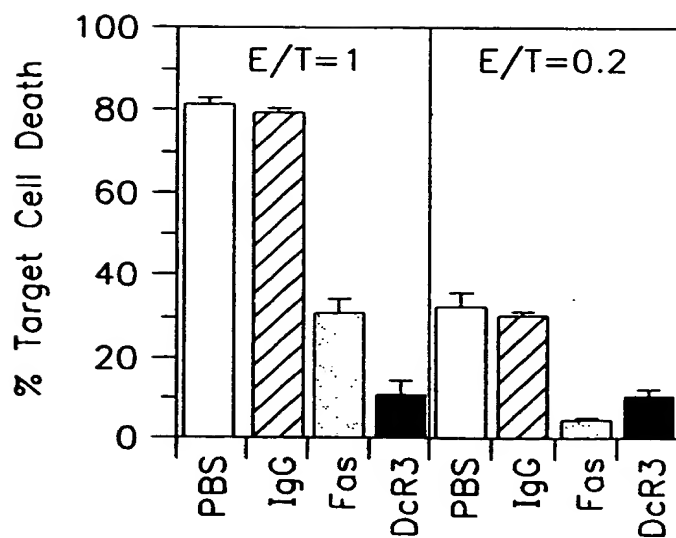


FIG. 9C

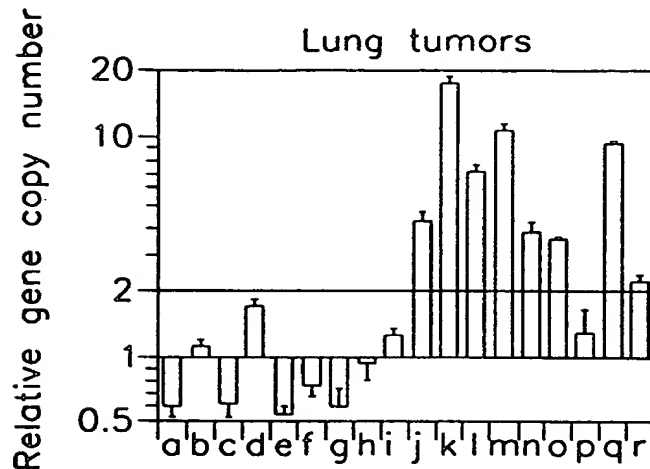


FIG. 10A

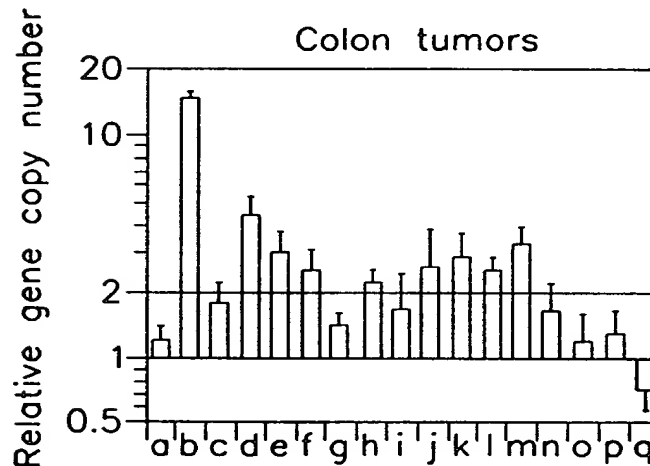


FIG. 10B

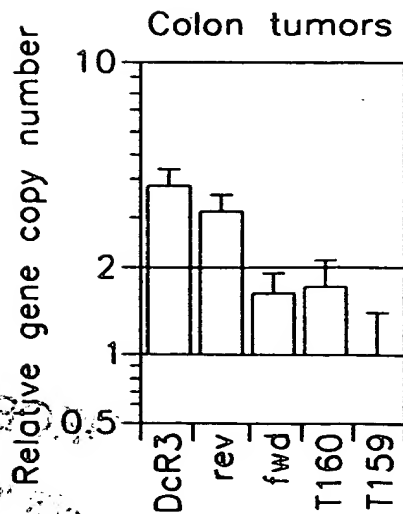


FIG. 10C

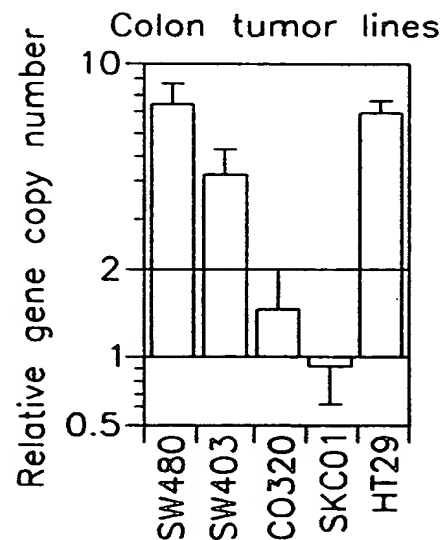


FIG. 10D

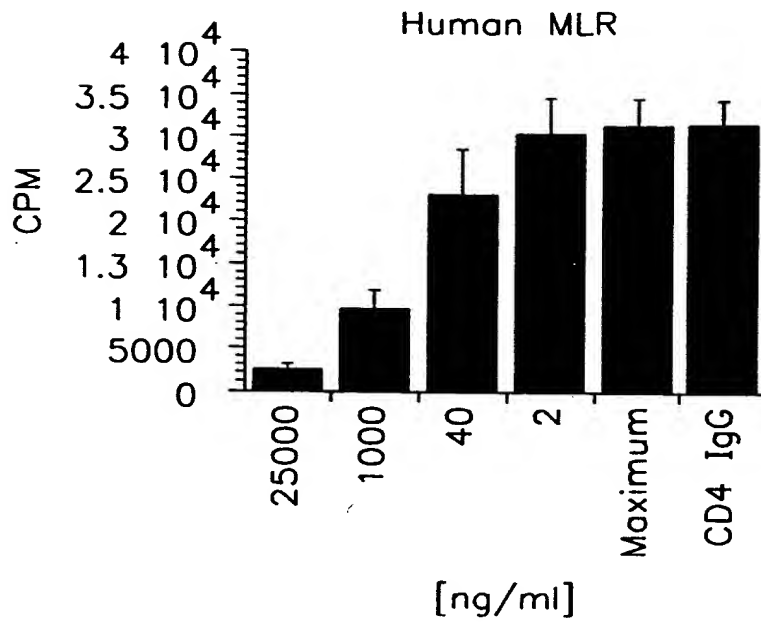


FIG. 1 IA

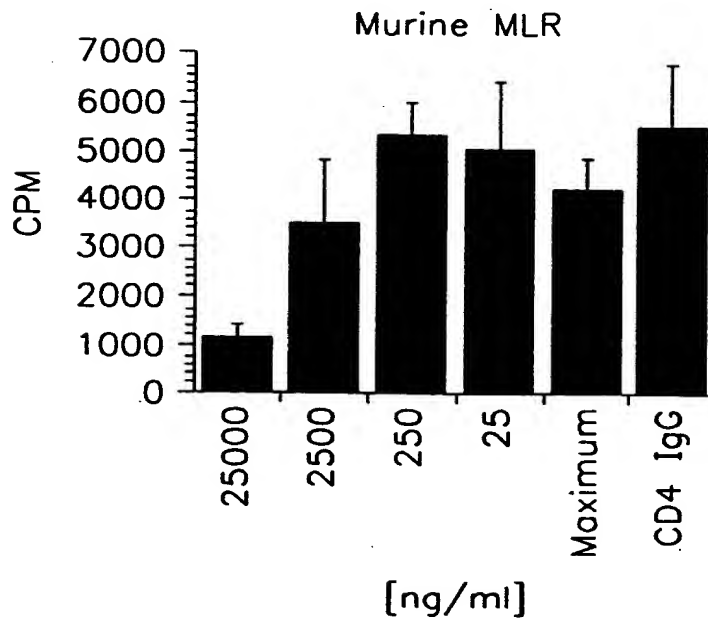


FIG. 1 IB

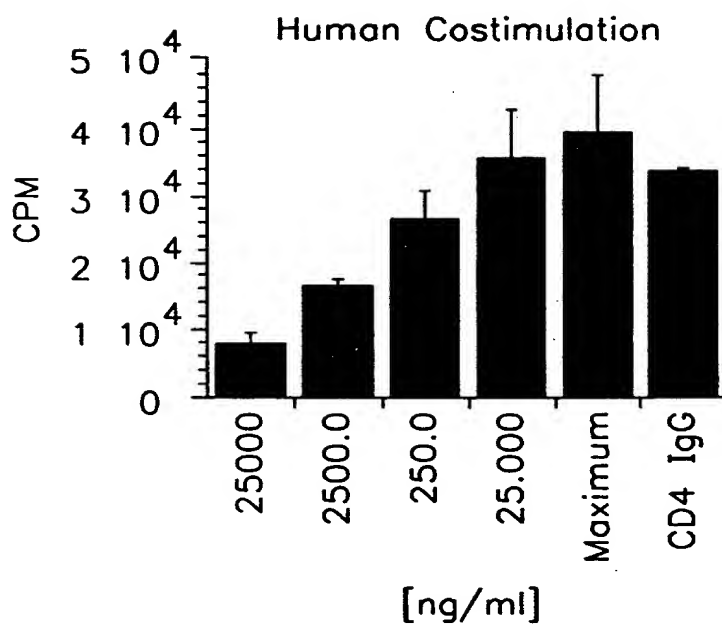


FIG. 1 IC



mAb	Isotype	Antigen Specificity (ELISA)					% Blocking (ELISA)
		DcR3	DR4	DR5	DcR1	OPG	
4B7.1.1	IgG1	+++	-	-	-	-	+
4C4.1.4	IgG2a	+++	-	-	-	-	-
5C4.14.7	IgG2b	+++	-	-	-	-	++
8D3.1.5	IgG1	+++	-	-	-	-	+/-
11C5.2.8	IgG1	+++	-	-	-	-	++

Antigen specificity was determined using 10 microgram/ml mAb.
 % blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

FIG. 12

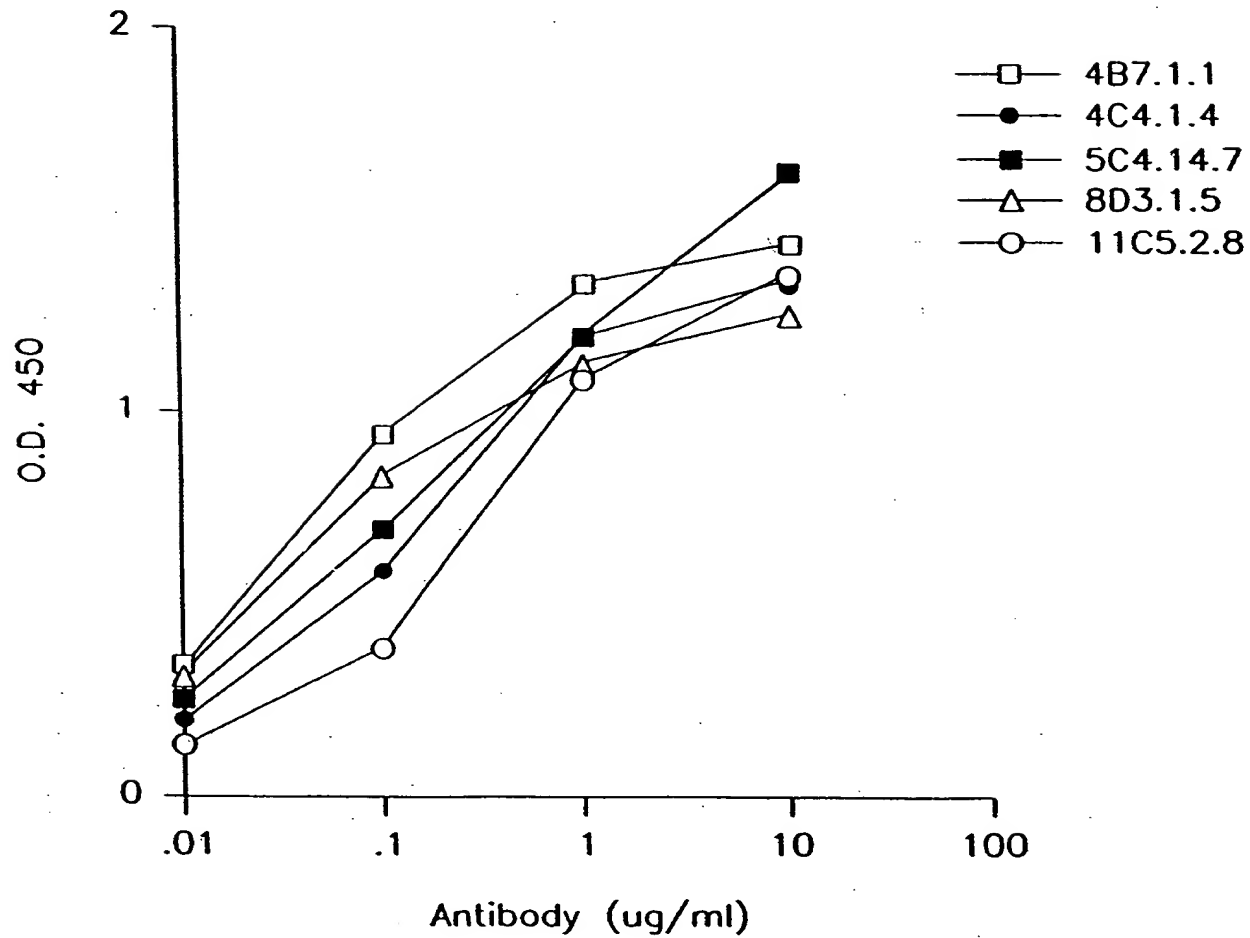


FIG. 13

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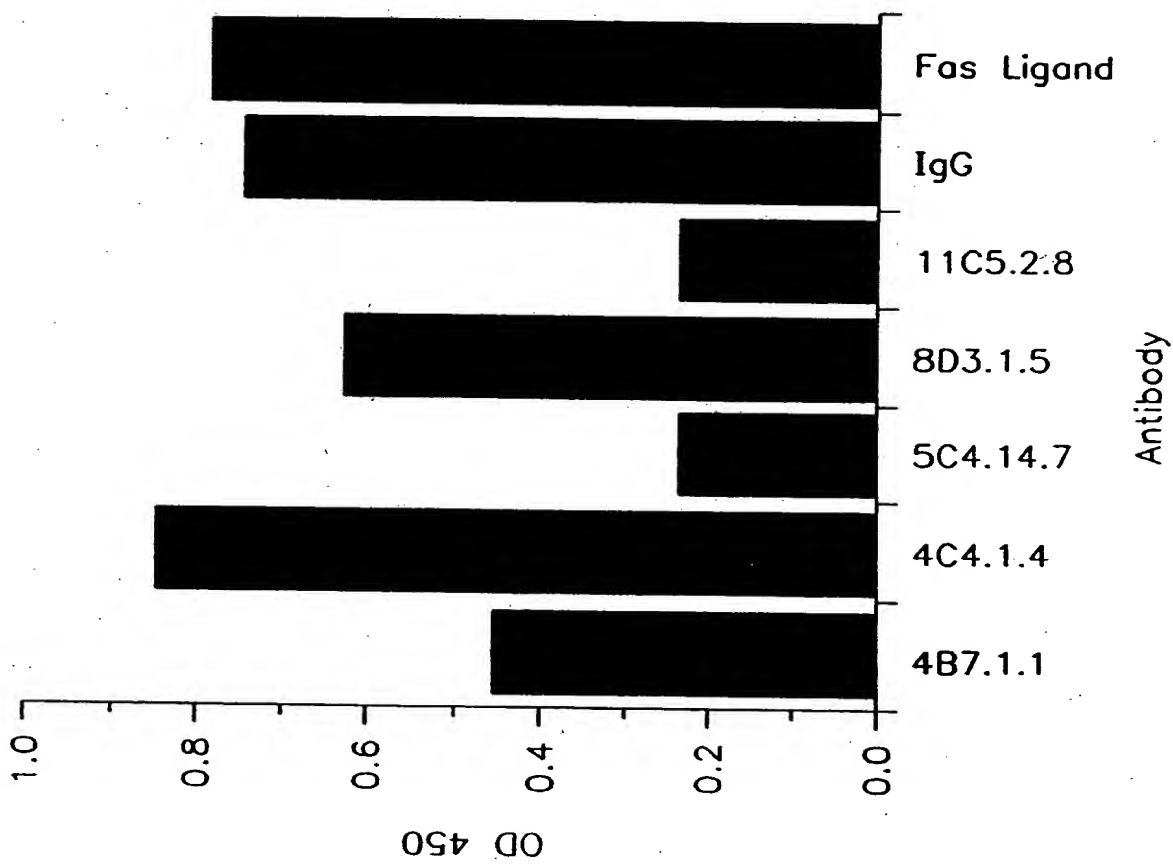


FIG. 14